

J. Roach

RUSH #11

ENTERED



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/728,420B

DATE: 06/03/2002

TIME: 13:08:11

Input Set : A:\A-579C.ST25.txt

Output Set: N:\CRF3\06032002\I728420B.raw

3 <110> APPLICANT: Yoshinaga, Steven
 4 Mak, Tak
 5 Shahinian, Arda
 6 Trafuri Bladt, Anna
 7 Senaldi, Giorgio
 9 <120> TITLE OF INVENTION: Polypeptides Involved in Immune Response
 11 <130> FILE REFERENCE: A-579C
 13 <140> CURRENT APPLICATION NUMBER: 09/728,420B
 C--> 14 <141> CURRENT FILING DATE: 2002-05-17
 16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
 17 <151> PRIOR FILING DATE: 2000-01-27
 19 <150> PRIOR APPLICATION NUMBER: US 09/264,527
 20 <151> PRIOR FILING DATE: 1999-03-08
 22 <150> PRIOR APPLICATION NUMBER: US 09/244,448
 23 <151> PRIOR FILING DATE: 1999-02-03
 25 <160> NUMBER OF SEQ ID NOS: 35
 27 <170> SOFTWARE: PatentIn version 3.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 600
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Mus musculus
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (1)..(600)
 38 <400> SEQUENCE: 1
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 41 1 5 10 15
 43 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca 96
 44 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 45 20 25 30
 47 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
 48 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 49 35 40 45
 51 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
 52 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 53 50 55 60
 55 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
 56 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
 57 65 70 75 80
 59 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288
 60 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 61 85 90 95

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63 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
64 Asn. Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
65          100          105          110
67 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat      384
68 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
69          115          120          125
71 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta      432
72 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
73          130          135          140
75 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata      480
76 Pro Val Gly Cys Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
77 145          150          155          160
79 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac      528
80 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
81          165          170          175
83 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag      576
84 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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93 <211> LENGTH: 200
94 <212> TYPE: PRT
95 <213> ORGANISM: Mus musculus
97 <400> SEQUENCE: 2
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104          20          25          30
107 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
108          35          40          45
111 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
112          50          55          60
115 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
116 65          70          75          80
119 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
120          85          90          95
123 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
124          100          105          110
127 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
128          115          120          125
131 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
132          130          135          140
135 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
136 145          150          155          160
139 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
140          165          170          175
143 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys

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156 <400> SEQUENCE: 3
158 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
159 1          5          10          15
161 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
162          20          25          30
164 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
165          35          40          45
167 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
168          50          55          60
170 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
171 65          70          75          80
173 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
174          85          90          95
176 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
177          100          105          110
179 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
180          115          120          125
182 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
183          130          135          140
185 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
186 145          150          155          160
188 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
189          165          170          175
191 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
192          180          185          190
194 Ser Arg Leu Ala Gly Val Thr Ser
195          195          200
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198 <211> LENGTH: 218
199 <212> TYPE: PRT
200 <213> ORGANISM: Mus musculus
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207 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
208          20          25          30
210 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
211          35          40          45
213 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
214          50          55          60
216 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
217 65          70          75          80

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219 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
220                               85                               90                               95
222 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
223                               100                              105                              110
225 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
226                               115                              120                              125
228 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
229                               130                              135                              140
231 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
232 145                               150                              155                              160
234 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
235                               165                              170                              175
237 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
238                               180                              185                              190
240 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
241                               195                              200                              205
243 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
244                               210                              215
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247 <211> LENGTH: 44
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_feature
253 <223> OTHER INFORMATION: Synthetic
256 <400> SEQUENCE: 5
258 Met Arg Leu Leu Val Ser Cys Tyr Leu Val Cys Cys Asn Val Phe Leu
259 1                               5                               10                               15
261 Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
262                               20                               25                               30
264 Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
265                               35                               40
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268 <211> LENGTH: 966
269 <212> TYPE: DNA
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272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)..(966)
276 <400> SEQUENCE: 6
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278 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
279 1                               5                               10                               15
281 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
282 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
283                               20                               25                               30
285 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act      144
286 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
287                               35                               40                               45

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289	gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac	192
290	Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp	
291	50 55 60	
293	ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa	240
294	Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln	
295	65 70 75 80	
297	atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct	288
298	Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser	
299	85 90 95	
301	cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc	336
302	Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser	
303	100 105 110	
305	ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc	384
306	Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val	
307	115 120 125	
309	acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca	432
310	Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr	
311	130 135 140	
313	gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg	480
314	Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val	
315	145 150 155 160	
317	gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac	528
318	Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn	
319	165 170 175	
321	ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca	576
322	Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro	
323	180 185 190	
325	gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac	624
326	Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp	
327	195 200 205	
329	acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat	672
330	Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr	
331	210 215 220	
333	gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt	720
334	Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val	
335	225 230 235 240	
337	ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att	768
338	Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile	
339	245 250 255	
341	agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa	816
342	Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu	
343	260 265 270	
345	acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg	864
346	Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu	
347	275 280 285	
349	gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc	912
350	Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro	
351	290 295 300	
353	cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac	960

VERIFICATION SUMMARY

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L:1303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21